

SEQUENCE LISTING

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<120> DEVELOPMENT OF MAMMALIAN GENOME MODIFICATION TECHNIQUE
 USING RETROTRANSPOSON

<130> 710048.401USPC

<140> US 10/579,936

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<160> 47

<170> PatentIn version 3.2

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<211> 7318

<212> DNA

<213> Mus musculus

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<223> IAP sequence actually used in the Examples for exemplification

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Gly Lys Pro Arg Leu	Leu Lys Thr Asp Asn	Gly Pro Ala Tyr Thr	
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Asn Glu Met Val Lys	Trp Lys Asn Val Leu	Asp Asn Lys Trp Tyr	
1565	1570	1575	
ggc ccg gat cct atc	ttg ata aga tcc agg	gga gct atc tgt gtt	5677
Gly Pro Asp Pro Ile	Leu Ile Arg Ser Arg	Gly Ala Ile Cys Val	
1580	1585	1590	
ttc cca cag aat gaa	gac aac cca ttt tgg	gta cca gaa aga ctc	5722
Phe Pro Gln Asn Glu	Asp Asn Pro Phe Trp	Val Pro Glu Arg Leu	
1595	1600	1605	
acc cga aaa atc cag	act gac caa ggg aat	act aat gtc cct cgt	5767
Thr Arg Lys Ile Gln	Thr Asp Gln Gly Asn	Thr Asn Val Pro Arg	
1610	1615	1620	
ctt ggt gat gtc cag	ggc gtc aat aat aaa	gag aga gca gcg ttg	5812
Leu Gly Asp Val Gln	Gly Val Asn Asn Lys	Glu Arg Ala Ala Leu	
1625	1630	1635	
ggg gat aat gtc gac	att tcc act ccc aat	gac ggt gat gta	5854
Gly Asp Asn Val Asp	Ile Ser Thr Pro Asn	Asp Gly Asp Val	

1640

1645

taatgctcaa	gtattctcct	gctttttttac	cactaactag	gaactggggtt	tggccttaat	5914
tcagacagcc	ttggctctgt	ctggacaggt	ccagatgact	gacaccatta	acactttgtc	5974
agcctcagtg	actacagtca	tagatgaaca	ggcctcagct	aatgtcaaga	tacagagagg	6034
tctcatgctg	gttaatcaac	tcatagatct	tgtccagaaa	caactggatg	tattatgaca	6094
aataactcag	cagggatgtg	aacaaaagtt	tccgggattg	tgtgttatatt	ccattcagta	6154
tgttaaattt	actaggacag	ctaatttgtc	aaaaagtctt	tttcagtata	tgttacagaa	6214
ttggatggct	gaatttgaat	agatccttcg	agaattgaga	cttcagggtca	actccacgcg	6274
cttggacctg	tcgctgacca	aaagattacc	caattggatc	tcctcagcat	tttctttctt	6334
taaaaaattg	ggtgggatta	atattatttg	gagatacact	ttgctgtgga	ttagtggtgc	6394
ttcttttgatt	ggtctgtaag	cttaaggccc	aaactaagag	agacaagggtg	gttattgccc	6454
aggcgcttgc	aggactagaa	catggagctt	cccctgatat	atctatgctt	aagcaatagg	6514
tcgctggcca	ctcagctctt	atatctcacg	aggctagtct	cattgcacga	gatagagtga	6574
gtgtgcttca	gcagcccgag	agagttgcaa	ggctaagcac	tgcagtagaa	gggctctgcg	6634
gcacatatga	gcctattcta	gggagacatg	tcattctttca	tgaagggttca	gtgtcctagt	6694
tcctttcccc	caggcaaaac	gacacgggag	caggtcaggg	ttgctctggg	taaaagcctg	6754
taagcctaag	agctaatect	gtacatggct	cctttaccta	cacactgggg	atttgacctc	6814
tatctccact	ctcathtaata	tgggtggcct	atttgctctt	attaaaagaa	aaagggggaa	6874
ctgtgggaag	ccgccccac	attcgccgtc	acaagatggc	gctgacatcc	tgtgttctaa	6934
gttggtaaac	aaataatctg	cgcattgagcc	aagggtatct	acgactactt	gtactctgtt	6994
tttcccgatga	acgtcagctc	ggccatgggc	tgcagccaat	cagggagtga	tgcgccctag	7054
gcaatgggtg	ttctctttta	aatagaaggg	gtttcggttt	tctcgctctc	ttgcttcttg	7114
ctctctcttg	cttccctctc	ttgcttcttg	ctctctcttg	cttccctctc	ttgcttcttg	7174
ctctctcttg	cttccctctc	ttgcttcttg	ctctctcttg	cttcttgctc	tcttttcctg	7234
aagatgtaag	aataaagctt	tgtcgcagaa	gattctgggc	tgtgggtgttc	ttcctggccg	7294
gtcgtgagaa	cgcgtcgaat	aaca				7318

<210> 2

<211> 586

<212> PRT

<213> Mus musculus

<220>

<223> IAP sequence amino acid sequence (gag #1)

<400> 2

Met	Asn	Ser	Glu	Leu	Phe	Ser	Trp	Gly	Thr	Arg	Val	Pro	Val	Ser	Met
1				5				10						15	
Phe	Gly	Leu	Glu	Phe	Phe	Leu	Val	Leu	Gly	Ala	Leu	Leu	Phe	Leu	Phe
			20					25					30		
Thr	Cys	Tyr	Ile	Val	Val	Lys	Ala	Gly	Leu	Lys	Ile	Leu	Asp	Glu	Ile
		35				40					45				
Gln	Gly	Ser	Leu	Ser	Glu	Val	Lys	Arg	Gly	Glu	Arg	Val	Gly	Ala	Arg
	50				55					60					
Arg	Asn	Gly	Lys	Tyr	Thr	Gly	Leu	Ser	Lys	Gly	Leu	Glu	Pro	Glu	Glu
65				70				75						80	
Lys	Leu	Arg	Leu	Gly	Arg	Asn	Thr	Trp	Arg	Glu	Ile	Arg	Arg	Lys	Arg
			85					90					95		
Gly	Lys	Arg	Glu	Lys	Lys	Lys	Asp	Arg	Leu	Ala	Glu	Val	Ser	Arg	Arg
			100					105					110		

Tyr	Ser	Ser	Leu	Asp	Glu	Leu	Arg	Lys	Pro	Ala	Leu	Ser	Ser	Ser	Glu
		115					120					125			
Ala	Ser	Glu	Glu	Ser	Ser	Ser	Glu	Glu	Thr	Asp	Trp	Glu	Glu	Glu	Ala
	130					135					140				
Ala	His	Tyr	Gln	Pro	Ala	Asn	Trp	Ser	Arg	Lys	Lys	Pro	Lys	Ala	Ala
145					150					155					160
Gly	Glu	Ser	Gln	Arg	Thr	Val	Gln	Pro	Pro	Gly	Ser	Arg	Phe	Gln	Gly
				165					170					175	
Pro	Pro	Tyr	Ala	Glu	Pro	Pro	Pro	Cys	Val	Val	Arg	Gln	Gln	Cys	Ala
			180					185					190		
Glu	Arg	Gln	Cys	Ala	Glu	Arg	Cys	Ala	Glu	Arg	Gln	Cys	Ala	Asp	Arg
		195					200					205			
Cys	Ala	Glu	Arg	Gln	Cys	Ala	Glu	Arg	Gln	Cys	Ala	Asp	Ser	Phe	Ile
	210					215					220				
Pro	Arg	Glu	Glu	Gln	Lys	Lys	Ile	Glu	Gln	Ala	Phe	Pro	Val	Phe	Glu
225					230					235					240
Gly	Ala	Glu	Gly	Gly	Arg	Val	His	Ala	Pro	Val	Glu	Tyr	Val	Gln	Ile
				245					250					255	
Lys	Glu	Ile	Ala	Glu	Ser	Val	Arg	Lys	Tyr	Gly	Thr	Asn	Ala	Asn	Phe
			260					265					270		
Thr	Leu	Val	Gln	Leu	Asp	Arg	Leu	Ala	Gly	Met	Ala	Leu	Thr	Pro	Ala
		275					280					285			
Asp	Trp	Gln	Thr	Val	Val	Lys	Ala	Ala	Leu	Pro	Ser	Met	Gly	Lys	Tyr
	290					295					300				
Met	Glu	Trp	Lys	Ala	Leu	Trp	His	Glu	Ala	Ala	Gln	Ala	Gln	Ala	Arg
305					310					315					320
Ala	Asn	Ala	Ala	Ala	Leu	Thr	Pro	Glu	Gln	Arg	Asp	Trp	Thr	Phe	Asp
				325					330					335	
Leu	Leu	Thr	Gly	Gln	Gly	Ala	Tyr	Ser	Ala	Asp	Gln	Thr	Asn	Tyr	His
			340					345					350		
Trp	Gly	Ala	Tyr	Ala	Gln	Ile	Ser	Ser	Thr	Ala	Ile	Arg	Ala	Trp	Lys
		355				360						365			
Ala	Leu	Ser	Arg	Ala	Gly	Glu	Thr	Thr	Gly	Gln	Leu	Thr	Lys	Ile	Ile
	370					375					380				
Gln	Gly	Pro	Gln	Glu	Ser	Phe	Ser	Asp	Phe	Val	Ala	Arg	Met	Thr	Glu
385					390					395					400
Ala	Ala	Glu	Arg	Ile	Phe	Gly	Glu	Ser	Glu	Gln	Ala	Ala	Pro	Leu	Ile

	405		410		415
Glu Gln Leu Ile Tyr Glu Gln Ala Thr Lys Glu Cys Arg Ala Ala Ile	420		425		430
Ala Pro Arg Lys Asn Lys Gly Leu Gln Asp Trp Leu Arg Val Cys Arg	435		440		445
Glu Leu Gly Gly Pro Leu Ser Asn Ala Gly Leu Ala Ala Ala Ile Leu	450		455		460
Gln Ser Gln Asn Arg Ser Met Gly Arg Asn Asp Gln Arg Thr Cys Phe	465		470		475
Asn Cys Gly Lys Pro Gly His Phe Lys Lys Asp Cys Arg Ala Pro Asp	485		490		495
Lys Gln Gly Gly Thr Leu Thr Leu Cys Ser Lys Cys Gly Lys Gly Tyr	500		505		510
His Arg Ala Asp Gln Cys Arg Ser Val Arg Asp Ile Lys Gly Arg Ile	515		520		525
Leu Pro Pro Pro Asp Ser Gln Ser Ala Asp Val Pro Lys Asn Gly Ser	530		535		540
Pro Gly Pro Arg Ser Gln Gly Pro Gln Arg Tyr Gly Asn Arg Phe Val	545		550		555
Arg Thr Gln Glu Ala Val Arg Glu Thr Thr Gln Glu Asp Pro Gln Gly	565		570		575
Trp Thr Cys Val Pro Pro Pro Thr Ser Tyr	580		585		

<210> 3
 <211> 258
 <212> PRT
 <213> Mus musculus

<220>
 <223> IAP sequence amino acid sequence (gag #2)

<400> 3

Met Pro Gln Met Ser Ile Gln Pro Val Pro Val Glu Pro Ile Pro Ser	1	5	10	15
Leu Pro Pro Gly Thr Met Gly Leu Ile Leu Gly Arg Gly Ser Leu Thr	20	25	30	
Leu Gln Gly Leu Val Val His Pro Gly Ile Met Asp Cys Gln His Ser	35	40	45	

Pro Glu Ile Gln Val Leu Cys Ser Ser Pro Lys Gly Val Phe Ser Ile
 50 55 60
 Ser Lys Gly Asp Arg Ile Ala Gln Leu Leu Leu Leu Pro Asp Asn Thr
 65 70 75 80
 Arg Glu Lys Ser Ala Gly Pro Glu Ile Lys Lys Met Gly Ser Ser Gly
 85 90 95
 Asn Asp Ser Ala Tyr Leu Val Val Ser Leu Asn Asp Arg Pro Lys Leu
 100 105 110
 Arg Leu Lys Ile Asn Gly Lys Glu Phe Glu Gly Ile Leu Asp Thr Gly
 115 120 125
 Ala Asp Lys Ser Ile Ile Ser Thr His Trp Trp Pro Lys Ala Trp Pro
 130 135 140
 Thr Thr Glu Ser Ser His Ser Leu Gln Gly Leu Gly Tyr Gln Ser Cys
 145 150 155 160
 Pro Thr Ile Ser Ser Val Ala Leu Thr Trp Glu Ser Ser Glu Gly Gln
 165 170 175
 Gln Gly Lys Phe Ile Pro Tyr Val Leu Pro Leu Pro Val Asn Leu Trp
 180 185 190
 Gly Arg Asp Ile Met Gln His Leu Gly Leu Ile Leu Ser Asn Glu Asn
 195 200 205
 Ala Pro Ser Gly Gly Tyr Ser Ala Lys Ala Lys Asn Ile Met Ala Lys
 210 215 220
 Met Gly Tyr Lys Glu Gly Lys Gly Leu Gly His Gln Glu Gln Gly Arg
 225 230 235 240
 Ile Glu Pro Ile Ser Pro Asn Gly Asn Gln Asp Arg Gln Gly Leu Gly
 245 250 255
 Phe Pro

<210> 4
 <211> 805
 <212> PRT
 <213> Mus musculus

<220>
 <223> IAP sequence amino acid sequence (pol)

<400> 4

Met	Asn	Leu	Phe	Gly	Pro	Val	Gln	Arg	Gly	Leu	Pro	Val	Leu	Ser	Ala	1	5	10	15
Leu	Pro	Arg	Gly	Trp	Asn	Leu	Ile	Ile	Ile	Asp	Ile	Lys	Asp	Cys	Phe	20	25	30	
Phe	Ser	Ile	Pro	Leu	Cys	Pro	Arg	Asp	Arg	Pro	Arg	Phe	Ala	Phe	Thr	35	40	45	
Ile	Pro	Ser	Ile	Asn	His	Met	Glu	Pro	Asp	Lys	Arg	Tyr	Gln	Trp	Lys	50	55	60	
Val	Leu	Pro	Gln	Gly	Met	Ser	Asn	Ser	Pro	Thr	Met	Cys	Gln	Leu	Tyr	65	70	75	80
Val	Gln	Glu	Ala	Leu	Leu	Pro	Val	Arg	Glu	Gln	Phe	Pro	Ser	Leu	Ile	85	90	95	
Leu	Leu	Leu	Tyr	Met	Asp	Asp	Ile	Leu	Leu	Cys	His	Lys	Asp	Leu	Thr	100	105	110	
Met	Leu	Gln	Lys	Ala	Tyr	Pro	Phe	Leu	Leu	Lys	Thr	Leu	Ser	Gln	Trp	115	120	125	
Gly	Leu	Gln	Ile	Ala	Thr	Glu	Lys	Val	Gln	Ile	Ser	Asp	Thr	Gly	Gln	130	135	140	
Phe	Leu	Gly	Ser	Val	Val	Ser	Pro	Asp	Lys	Ile	Val	Pro	Gln	Lys	Val	145	150	155	160
Glu	Ile	Arg	Arg	Asp	His	Leu	His	Thr	Leu	Asn	Asp	Phe	Gln	Lys	Leu	165	170	175	
Leu	Gly	Asp	Ile	Asn	Trp	Leu	Arg	Pro	Phe	Leu	Lys	Ile	Pro	Ser	Ala	180	185	190	
Glu	Leu	Arg	Pro	Leu	Phe	Ser	Ile	Leu	Glu	Gly	Asp	Pro	His	Ile	Ser	195	200	205	
Ser	Pro	Arg	Thr	Leu	Thr	Leu	Ala	Ala	Asn	Gln	Ala	Leu	Gln	Lys	Val	210	215	220	
Glu	Lys	Ala	Leu	Gln	Asn	Ala	Gln	Leu	Gln	Arg	Ile	Glu	Asp	Ser	Gln	225	230	235	240
Pro	Phe	Ser	Leu	Cys	Val	Phe	Lys	Thr	Ala	Gln	Leu	Pro	Thr	Ala	Val	245	250	255	
Leu	Trp	Gln	Asn	Gly	Pro	Leu	Leu	Trp	Ile	His	Pro	Asn	Val	Ser	Pro	260	265	270	
Ala	Lys	Ile	Ile	Asp	Trp	Tyr	Pro	Asp	Ala	Ile	Ala	Gln	Leu	Ala	Leu				

275					280					285					
Lys	Gly	Leu	Lys	Ala	Ala	Ile	Thr	His	Phe	Gly	Gln	Ser	Pro	Tyr	Leu
290						295					300				
Leu	Ile	Val	Pro	Tyr	Thr	Ala	Ala	Gln	Val	Gln	Thr	Leu	Ala	Ala	Ala
305					310					315					320
Ser	Asn	Asp	Trp	Ala	Val	Leu	Val	Thr	Ser	Phe	Ser	Gly	Lys	Ile	Asp
				325					330					335	
Asn	His	Tyr	Pro	Lys	His	Pro	Ile	Leu	Gln	Phe	Ala	Gln	Asn	Gln	Ser
			340					345					350		
Val	Val	Phe	Pro	Gln	Ile	Thr	Val	Arg	Asn	Pro	Leu	Lys	Asn	Gly	Ile
		355					360					365			
Val	Val	Tyr	Thr	Asp	Gly	Ser	Lys	Thr	Gly	Ile	Gly	Ala	Tyr	Val	Ala
		370				375					380				
Asn	Gly	Lys	Val	Val	Ser	Lys	Gln	Tyr	Asn	Glu	Asn	Ser	Pro	Gln	Val
385					390					395					400
Val	Glu	Cys	Leu	Val	Val	Leu	Glu	Val	Leu	Lys	Thr	Phe	Leu	Lys	Pro
			405						410					415	
Leu	Asn	Ile	Val	Ser	Asp	Ser	Cys	Tyr	Val	Val	Asn	Ala	Val	Asn	Leu
			420					425					430		
Leu	Glu	Val	Ala	Gly	Val	Ile	Lys	Pro	Ser	Ser	Arg	Val	Ala	Asn	Ile
		435					440					445			
Phe	Gln	Gln	Ile	Gln	Leu	Val	Leu	Leu	Ser	Arg	Arg	Ser	Pro	Val	Tyr
					455						460				
Ile	Thr	His	Val	Arg	Ala	His	Ser	Gly	Leu	Pro	Gly	Pro	Met	Ala	Leu
465					470					475					480
Gly	Asn	Asp	Leu	Ala	Asp	Lys	Ala	Thr	Lys	Val	Val	Ala	Ala	Ala	Leu
				485					490					495	
Ser	Ser	Pro	Val	Glu	Ala	Ala	Arg	Asn	Phe	His	Asn	Asn	Phe	His	Val
			500					505					510		
Thr	Ala	Glu	Thr	Leu	Arg	Ser	Arg	Phe	Ser	Leu	Thr	Arg	Lys	Glu	Ala
		515					520					525			
Arg	Asp	Ile	Val	Thr	Gln	Cys	Gln	Ser	Cys	Cys	Glu	Phe	Leu	Pro	Val
	530					535					540				
Pro	His	Val	Gly	Ile	Asn	Pro	Arg	Gly	Ile	Arg	Pro	Leu	Gln	Val	Trp
545					550					555					560
Gln	Met	Asp	Val	Thr	His	Val	Ser	Ser	Phe	Gly	Lys	Leu	Gln	Tyr	Leu

565					570					575					
His	Val	Ser	Ile	Asp	Thr	Cys	Ser	Gly	Ile	Met	Phe	Ala	Ser	Pro	Leu
			580					585					590		
Thr	Gly	Glu	Lys	Ala	Ser	His	Val	Ile	Gln	His	Cys	Leu	Glu	Ala	Trp
		595					600					605			
Ser	Ala	Trp	Gly	Lys	Pro	Arg	Leu	Leu	Lys	Thr	Asp	Asn	Gly	Pro	Ala
	610					615					620				
Tyr	Thr	Ser	Gln	Lys	Phe	Gln	Gln	Phe	Cys	Arg	Gln	Met	Asp	Val	Thr
625					630					635					640
His	Leu	Thr	Gly	Leu	Pro	Tyr	Asn	Pro	Gln	Gly	Gln	Gly	Ile	Val	Glu
				645					650					655	
Arg	Ala	His	Arg	Thr	Leu	Lys	Ala	Tyr	Leu	Ile	Lys	Gln	Lys	Arg	Gly
			660					665					670		
Thr	Phe	Glu	Glu	Thr	Val	Pro	Arg	Ala	Pro	Arg	Val	Ser	Val	Ser	Leu
		675					680					685			
Ala	Leu	Phe	Thr	Leu	Asn	Phe	Leu	Asn	Ile	Asp	Ala	His	Gly	His	Thr
	690					695					700				
Ala	Ala	Glu	Arg	His	Cys	Ser	Glu	Pro	Asp	Arg	Pro	Asn	Glu	Met	Val
705					710					715					720
Lys	Trp	Lys	Asn	Val	Leu	Asp	Asn	Lys	Trp	Tyr	Gly	Pro	Asp	Pro	Ile
				725					730					735	
Leu	Ile	Arg	Ser	Arg	Gly	Ala	Ile	Cys	Val	Phe	Pro	Gln	Asn	Glu	Asp
			740					745					750		
Asn	Pro	Phe	Trp	Val	Pro	Glu	Arg	Leu	Thr	Arg	Lys	Ile	Gln	Thr	Asp
		755					760					765			
Gln	Gly	Asn	Thr	Asn	Val	Pro	Arg	Leu	Gly	Asp	Val	Gln	Gly	Val	Asn
	770					775					780				
Asn	Lys	Glu	Arg	Ala	Ala	Leu	Gly	Asp	Asn	Val	Asp	Ile	Ser	Thr	Pro
785					790					795					800
Asn	Asp	Gly	Asp	Val											
				805											

<210> 5
 <211> 673
 <212> DNA
 <213> Mus musculus

<220>

<223> CMV promoter sequence

<400> 5

tggccattgc	atacgttgta	tccatatcat	aatatgtaca	tttatattgg	ctcatgtcca	60
acattaccgc	catgttgaca	ttgattattg	actagttatt	aatagtaatc	aattacgggg	120
tcattagttc	atagcccata	tatggagttc	cgcattacat	aacttacggg	aaatggccc	180
cctggctgac	cgcccaacga	ccccgccc	ttgacgtcaa	taatgacgta	tgttcccata	240
gtaacgcaa	tagggacttt	ccattgacgt	caatgggtgg	agtatttacg	gtaaactgcc	300
cacttggcag	tacatcaagt	gtatcatatg	ccaagtacgc	cccctattga	cgtcaatgac	360
ggtaaattgg	ccgcctggca	ttatgccag	tacatgacct	tatgggactt	tcctacttgg	420
cagtacatct	acgtattagt	catcgctatt	accatgggtga	tgcgggtttg	gcagtacatc	480
aatgggcgtg	gatagcggtt	tgactcacgg	ggatttccaa	gtctccaccc	cattgacgtc	540
aatgggagtt	tgttttggca	ccaaaatcaa	cgggactttc	caaaatgtcg	taacaactcc	600
gccccattga	cgcaaatggg	cggtaggcgt	gtacgggtggg	aggtctatat	aagcagagct	660
cgttttagtga	acc					673

<210> 6

<211> 655

<212> DNA

<213> Mus musculus

<220>

<223> CA1 promoter sequence (without the R region and with two bases deletion in the promoter region in addition thereto)

<400> 6

attgattatt	gactagttat	taatagtaat	caattacggg	gtcattagtt	catagcccat	60
atatggagtt	ccgcgttaca	taacttacgg	taaatggccc	gcctggctga	ccgcccacg	120
acccccgccc	attgacgtca	ataatgacgt	atgttcccat	agtaacgcca	atagggactt	180
tccattgacg	tcaatgggtg	gactattttac	ggtaaactgc	ccacttggca	gtacatcaag	240
tgtatcatat	gccaaagtacg	ccccctattg	acgtcaatga	cggtaaattgg	cccgcctggc	300
attatgccca	gtacatgacc	ttatgggact	ttcctacttg	gcagtacatc	tacgtattag	360
tcacgcgtat	taccatgggt	cgaggtgagc	cccacgttct	gcttcactct	ccccatctcc	420
ccccctccc	caccccccaat	tttgtattta	tttatttttt	aattattttt	tgcagcgatg	480
ggggcggggg	gggggggggc	gcgcgccagg	cggggcgggg	cggggcgagg	ggcggggcg	540
ggcgaggcgg	agaggtgcgg	cggcagccaa	tcagagcggc	gcgctccgaa	agtttccttt	600
tatggcgagg	cggcgggcgg	ggcgggcccta	taaaaagcga	agcgcgcggc	ggg	655

<210> 7

<211> 657

<212> DNA

<213> Mus musculus

<220>

<223> CA2 promoter sequence (without the R region)

<400> 7

attgattatt	gactagttat	taatagtaat	caattacggg	gtcattagtt	catagcccat	60
atatggagtt	ccgcgttaca	taacttacgg	taaatggccc	gcctggctga	ccgcccacg	120
acccccgccc	attgacgtca	ataatgacgt	atgttcccat	agtaacgcca	atagggactt	180
tccattgacg	tcaatgggtg	gactattttac	ggtaaactgc	ccacttggca	gtacatcaag	240
tgtatcatat	gccaaagtacg	ccccctattg	acgtcaatga	cggtaaattgg	cccgcctggc	300

```

attatgccca gtacatgacc ttatgggact ttcctacttg gcagtacatc tacgtattag 360
tcatcgctat taccatgggt cgaggtgagc cccacgttct gcttcactct ccccatctcc 420
ccccctccc caccccaat tttgtattta tttatTTTTT aattatTTTg tgcagcgatg 480
ggggcggggg gggggggggc gcgcgccagg cggggcgggg cggggcgagg ggcggggcgg 540
ggcgaggcgg agaggtgcgg cggcagccaa tcagagcggc gcgctccgaa agtttccttt 600
tatggcgagg cggcgggcgg gcggggcccta taaaaagcga agcgcgcggc gggcggg 657

```

```

<210> 8
<211> 278
<212> DNA
<213> Gallus gallus

```

```

<220>
<223> avian beta-actin promoter sequence

```

```

<400> 8
tcgaggtgag cccacgttct tgcttcactc tcccatctc cccccctcc ccacccccaa 60
ttttgtattt atttatTTTT taattatTTT gtgcagcgat gggggcgggg gggggggggg 120
cgcgcgccag gcggggcggg gcggggcgag gggcggggag gggcgaggcg gagaggtgcg 180
gcggcagcca atcagagcgg cgcgctccga aagtttcctt ttatggcgag gcggcgggcg 240
cggcgggcct ataaaaagcg aagcgcgcgg cgggcggg 278

```

```

<210> 9
<211> 41
<212> DNA
<213> Mus musculus

```

```

<220>
<223> forward primer sequence for isolation of the IAP element used
      in Example 1

```

```

<400> 9
gcagcgggcg ccgtggtggc acacactttt agtccccgca g 41

```

```

<210> 10
<211> 41
<212> DNA
<213> Mus musculus

```

```

<220>
<223> reverse primer sequence for isolation of the IAP element used
      in Example 1

```

```

<400> 10
ggcgactag tgatgccctc tcaggcctcc actcaggcac t 41

```

```

<210> 11
<211> 30
<212> DNA
<213> Mus musculus

```

<220>
 <223> forward primer sequence for isolation of the full length of the IAP
 element used in Example 1

<400> 11
 atgccagat ttcttccacg gctattaggg 30

<210> 12
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>
 <223> reverse primer sequence for isolation of the full length of the IAP
 element used in Example 1

<400> 12
 gatgccctct caggcctcca ctcaggcact 30

<210> 13
 <211> 40
 <212> DNA
 <213> Mus musculus

<220>
 <223> forward primer sequence related to the CMV promoter used
 in Example 1 (c)

<400> 13
 ccaagcggcc gctggccatt gcatacgttg tatccatatac 40

<210> 14
 <211> 40
 <212> DNA
 <213> Mus musculus

<220>
 <223> reverse primer sequence related to the CMV promoter used
 in Example 1 (c)

<400> 14
 gcgagaaaaa cggttcacta aacgagctct gcttatatag 40

<210> 15
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>

<223> forward primer sequence related to the R region of the IAP used in Example 1 (c)

<400> 15
ttagtgaacc gtttttctcg ctctcttgct 30

<210> 16
<211> 30
<212> DNA
<213> Mus musculus

<220>
<223> reverse primer sequence related to the R region of the IAP used in Example 1 (c)

<400> 16
tctgaaatga agtatccctc ctgcgccagt 30

<210> 17
<211> 63
<212> DNA
<213> Mus musculus

<220>
<223> a linking sequence of a linker DNA used in Example 3

<400> 17
cgaatcgtaa ccgttcgtac gagaattcgt acgagaatcg ctgtcctctc caacgagcca 60

agg 63

<210> 18
<211> 26
<212> DNA
<213> Mus musculus

<220>
<223> a linking sequence of a linker DNA used in Example 3

<400> 18
ccttggctcg tttttttttg caaaaa 26

<210> 19
<211> 25
<212> DNA
<213> Mus musculus

<220>
<223> a linker specific primer for use in the first round in Example 3 (forward)

<400> 19
cgaatcgtaa ccgttcgtac gagaa

25

<210> 20
<211> 30
<212> DNA
<213> Mus musculus

<220>
<223> a linker specific primer for use in the first round
in Example 3 (reverse)

<400> 20
gagatgcatg ctttgcatac ttctgcctgc

30

<210> 21
<211> 25
<212> DNA
<213> Mus musculus

<220>
<223> a linker specific primer for use in the second round
in Example 3 (forward)

<400> 21
tcgtacgaga atcgctgtcc tctcc

25

<210> 22
<211> 30
<212> DNA
<213> Mus musculus

<220>
<223> a linking sequence of neo cassette specific primer for use
in the second round in Example 3 (reverse)

<400> 22
ggagcctggg gactttccac acctggttgc

30

<210> 23
<211> 30
<212> DNA
<213> Mus musculus

<220>
<223> an alternative linking sequence of neo cassette specific primer
for use in the second round in Example 3 (reverse)

<400> 23

ggggagcctg gggactttcc acaccctaac

30

<210> 24
 <211> 39
 <212> DNA
 <213> Gallus gallus

<220>
 <223> a primer 5' upstream until the transcription initiation site of
 chicken beta-actin promoter used in Example 4

<400> 24
 gcaatgcggc cgcattgatt attgactagt tattaatag

39

<210> 25
 <211> 39
 <212> DNA
 <213> Gallus gallus

<220>
 <223> a primer 3' of chicken beta-actin promoter used in Example 4

<400> 25
 cgagaaaaac cgcccgccgc gcgcttcgct ttttatagg

39

<210> 26
 <211> 40
 <212> DNA
 <213> Gallus gallus

<220>
 <223> an alternative primer 3' of chicken beta-actin promoter used
 in Example 4

<400> 26
 cgagaaaaac cccgcccgc gcgcgcttcg ctttttatag

40

<210> 27
 <211> 36
 <212> DNA
 <213> Mus musculus

<220>
 <223> a primer of the 5' upstream from the 5' terminus of the R region of
 the IAP to the downstream of the U5 region used in Example 4

<400> 27
 cgcggcgggc gggtttttctc gctctcttgc ttcttg

36

<210> 28
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>

<223> a primer of the 3' side from the 5' terminus of the R region of the IAP

to the downstream of the U5 region used in Example 4

<400> 28
 tctgaaatga agtatccctc ctgcgccagt

30

<210> 29
 <211> 36
 <212> DNA
 <213> Mus musculus

<220>

<223> an alternative primer of the 3' side from the 5' terminus of the R region of the IAP to the downstream of the U5 region used in Example 4

<400> 29
 cggcgggcgg ggtttttctc gctctcttgct ttcttg

36

<210> 30
 <211> 903
 <212> DNA
 <213> Mus musculus

<220>

<223> gamma globin intron sequence

<400> 30

gtgagtcacag	gagatgtttc	agcactgttg	ccttttagtct	cgaggcaact	tagacaactg	60
agtattgatc	tgagcacagc	agggtgtgag	ctgtttgaag	atactggggg	tgggggtgaa	120
gaaactgcag	aggactaact	gggctgagac	ccagtggcaa	tgttttaggg	cctaaggaat	180
gcctctgaaa	atctagatgg	acaactttga	ctttgagaaa	agagaggtgg	aaatgaggaa	240
aatgactttt	ctttattaga	tttcggtaga	aagaactttc	acctttcccc	tatttttggt	300
attcgtttta	aaacatctat	ctggaggcag	gacaagtatg	gtcgttaaaa	agatgcaggc	360
agaaggcata	tattggctca	gtcaaagtgg	gggaactttg	gtggccaaac	atacattgct	420
aaggctattc	ctatatcagc	tggacacata	taaaatgctg	ctaattgctt	attacaaact	480
tatatccttt	aattccagat	gggggcaaag	tatgtccagg	ggtgaggaac	aattgaaaca	540
tttgggctgg	agtagatttt	gaaagtcagc	tctgtgtgtg	tgtgtgtgtg	tgtgtgtgtg	600
tgtgtgtgcg	cgcacgtgtg	tttgtgtgtg	tgtgagagcg	tgtgtttctt	ttaacgtttt	660
cagcctacag	catacagggt	tcatgggtgg	aagaagataa	caagatttaa	attatggcca	720
gtgactagtg	ctgcaagaag	aacaactacc	tgcatttaat	gggaaagcaa	aatctcaggc	780
tttgagggaa	gttaacatag	gcttgattct	gggtggaagc	tgggtgtgta	gttatctgga	840
ggccaggctg	gagctctcag	ctcactatgg	gttcactctt	attgtctcct	ttcatctcaa	900
cag						903

<210> 31
 <211> 15
 <212> DNA
 <213> Mus musculus

<220>
 <223> a sequence of the tRNA binding site of the full length IAP

<400> 31
 tccgggacga gaaaa 15

<210> 32
 <211> 15
 <212> DNA
 <213> Mus musculus

<220>
 <223> a repeat sequence of the R region of the full length IAP

<400> 32
 ttgcttcttg ctctc 15

<210> 33
 <211> 17
 <212> DNA
 <213> Mus musculus

<220>
 <223> a specific sequence for the full length IAP (tRNA binding site)

<400> 33
 tgggtgccgaa ttccggg 17

<210> 34
 <211> 15
 <212> DNA
 <213> Mus musculus

<220>
 <223> a tandem repeat sequence specific for the full length IAP

<400> 34
 aatccgggac gagaa 15

<210> 35
 <211> 11
 <212> DNA
 <213> Mus musculus

<220>

<223> a repeat sequence of the R region found in the full length IAP

<400> 35

ttgcttcttg c

11

<210> 36

<211> 378

<212> DNA

<213> Mus musculus

<220>

<223> cytomegalovirus (CMV) enhancer sequence

<400> 36

attgattatt	gactagttat	taatagtaat	caattacggg	gtcattagtt	catagcccat	60
atatggagtt	ccgcgttaca	taacttacgg	taaatggccc	gcctggctga	ccgcccacg	120
acccccgccc	attgacgtca	ataatgacgt	atgttcccat	agtaacgcca	atagggactt	180
tccattgacg	tcaatgggtg	gagtatttac	ggtaaactgc	ccacttggca	gtacatcaag	240
tgtatcatat	gccaaagtacg	ccccctattg	acgtcaatga	cggtaaattg	cccgcctggc	300
attatgccca	gtacatgacc	ttatgggact	ttcctacttg	gcagtacatc	tacgtattag	360
tcacgcctat	taccatgg					378

<210> 37

<211> 30

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence in the sense direction of 1st primer used
in Example 8

<400> 37

agggctgcgg caagggcaac atcctgttcg

30

<210> 38

<211> 30

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence in the antisense direction of 1st primer used
in Example 8

<400> 38

gccgccgtcc tccacgtagg tcttctccag

30

<210> 39

<211> 30

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence in the sense direction of 2nd primer used
in Example 8

<400> 39

ggcaaccagc tggcgcagat ccgcgtgacc

30

<210> 40

<211> 30

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence in the antisense direction of 2nd primer used
in Example 8

<400> 40

gtccttcacc acgcccttgc tcttcacacag

30

<210> 41

<211> 37

<212> DNA

<213> unknown

<220>

<223> the sequence of a junctional portion between the
CMV promoter and the R region

<400> 41

gagctcgctt agtgaaccgt tttctcgct ctcttgc

37

<210> 42

<211> 36

<212> DNA

<213> UNKNOWN

<220>

<223> the sequence of a juncture site of CA promoter

<400> 42

gaagcgcgcg gcgggcgggt tttctcgctc tcttgc

36

<210> 43

<211> 38

<212> DNA

<213> unknown

<220>

<223> the sequence of a juncture site of CA promoter

<400> 43
gaagcgcgcg gcgggcgggg tttttctcgc tctcttgc

38

<210> 44
<211> 60
<212> DNA
<213> UNKNOWN

<220>
<223> Sequence of the GAG gene preferable for
transposition

<400> 44
atgaattcag aacttttcac gtggggaacg agagtaccag tgagtatgtt tggccttgaa 60

<210> 45
<211> 20
<212> PRT
<213> UNKNOWN

<220>
<223> Sequence of the GAG gene preferable for
transposition

<400> 45
Met Asn Ser Glu Leu Phe Ser Trp Gly Thr Arg Val Pro Val Ser Met
1 5 10 15
Phe Gly Leu Glu
20

<210> 46
<211> 15
<212> DNA
<213> unknown

<220>
<223> repeat sequence

<400> 46
tccgggacga gaaaa

15

<210> 47
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> repeat sequence

<400> 47
ttgcttcttg ctctc

15